RAW SEQUENCE LISTING
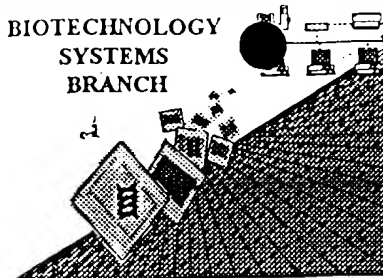# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/875,519_

Source: _0 IPE_

Date Processed by STIC: _9/6/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/875,519

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length.

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) /6 _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/875,519

DATE: 09/06/2001
TIME: 10:53:03

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\09062001\I875519.raw**

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   5 <110> APPLICANT: Farries, Timothy C.
   7         Harrison, Richard A.
  11 <120> TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
  15 <130> FILE REFERENCE: 4-30443/A/IMU/PCT
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/875,519
C--> 21 <141> CURRENT FILING DATE: 2001-06-06
  25 <150> PRIOR APPLICATION NUMBER: PCT/GB97/00603
  27 <151> PRIOR FILING DATE: 1997-03-04
  31 <160> NUMBER OF SEQ ID NOS: 35
  35 <170> SOFTWARE: PatentIn Ver. 2.0
  39 <210> SEQ ID NO: 1
  41 <211> LENGTH: 41
  43 <212> TYPE: DNA
  45 <213> ORGANISM: Artificial Sequence
  49 <220> FEATURE:
  51 <223> OTHER INFORMATION: Description of Artificial Sequence:
  53        oligodeoxynucleotide PL-ATC-3
  57 <400> SEQUENCE: 1
  59 tagggagacc ggaagcttgc cctctccctc tgtccctctg t              41
  63 <210> SEQ ID NO: 2
  65 <211> LENGTH: 30
  67 <212> TYPE: DNA
  69 <213> ORGANISM: Artificial Sequence
  73 <220> FEATURE:
  75 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
  77        oligodeoxynucleotide QRI1
  81 <400> SEQUENCE: 2
  83 caactgccca gccaaagctc caagatcacc                           30
  87 <210> SEQ ID NO: 3
  89 <211> LENGTH: 30
  91 <212> TYPE: DNA
  93 <213> ORGANISM: Artificial Sequence
  97 <220> FEATURE:
  99 <223> OTHER INFORMATION: Description of Artificial Sequence:
 101        oligodeoxynucleotide QRI2
 105 <400> SEQUENCE: 3
 107 gccagcctcc tgcaatcaga agagaccaag                           30
 111 <210> SEQ ID NO: 4
 113 <211> LENGTH: 32
 115 <212> TYPE: DNA
 117 <213> ORGANISM: Artificial Sequence
 121 <220> FEATURE:
 123 <223> OTHER INFORMATION: Description of Artificial Sequence:
 125        oligodeoxynucleotide AFL4149
 129 <400> SEQUENCE: 4
 131 taataaattc gaccttaagg tcaccataaa ac                        32
 135 <210> SEQ ID NO: 5
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137 <211> LENGTH: 30
139 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
147 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense
-149   oligodeoxynucleotide QRI1n
153 <400> SEQUENCE: 5
155 ggtgatcttg gagctttggc tgggcagttg   30
159 <210> SEQ ID NO: 6
161 <211> LENGTH: 30
163 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence:
173   antisense oligodeoxynucleotide
175   QRI2n
179 <400> SEQUENCE: 6
181 cttggtctct tctgattgca ggaggctggc   30
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187 <211> LENGTH: 32
189 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: antisense
199   oligonucleotide AFL4149n
203 <400> SEQUENCE: 7
205 gttttatggt gaccttaagg tcgaatttat ta   32
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211 <211> LENGTH: 30
213 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
223   primer
227 <400> SEQUENCE: 8
229 caactgccca gckrsagctc caagatcacc   30
233 <210> SEQ ID NO: 9
235 <211> LENGTH: 30
237 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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255 <210> SEQ ID NO: 10
257 <211> LENGTH: 32
259 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/875,519

DATE: 09/06/2001
TIME: 10:53:03

Input Set : A:\ES.txt
Output Set: N:\CRF3\09062001\I875519.raw

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271 <400> SEQUENCE: 10
273 gttttatggt gaccttaagg tcgaatttat ta                          32
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279 <211> LENGTH: 45
281 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
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289 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
291        oligonucleotide
295 <400> SEQUENCE: 11
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301 <210> SEQ ID NO: 12
303 <211> LENGTH: 39
305 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
315        oligonucleotide
319 <400> SEQUENCE: 12
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325 <210> SEQ ID NO: 13
327 <211> LENGTH: 44
329 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
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337 tgggtgcccc aaccatcatc atcatcatca ttgaccacac cccc             44
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345 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
353 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
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369 <212> TYPE: DNA
371 <213> ORGANISM: Artificial Sequence
375 <220> FEATURE:
377 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
381 <400> SEQUENCE: 15
383 tgtcatcgtg ccgctaaaga                                        20
387 <210> SEQ ID NO: 16
389 <211> LENGTH: 20
391 <212> TYPE: DNA
393 <213> ORGANISM: Artificial Sequence
W--> 397 <220> FEATURE:
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see item // on Error Summary Sheet

Input Set : A:\ES.txt
Output Set: N:\CRF3\09062001\I875519.raw

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     407 <212> TYPE: DNA
     409 <213> ORGANISM: Homo sapiens
     413 <400> SEQUENCE: 17
     415 aacggctgaa catattaatt cataccccct cgggc                 35
     419 <210> SEQ ID NO: 18
     421 <211> LENGTH: 33
     423 <212> TYPE: DNA
     425 <213> ORGANISM: Artificial Sequence
     429 <220> FEATURE:
     431 <223> OTHER INFORMATION: Description of Artificial Sequence: mutagenic
     433       primer
     437 <400> SEQUENCE: 18
     439 atctcgctgc gcaaggcttt cgatatttgc gag                   33
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     447 <212> TYPE: DNA
     449 <213> ORGANISM: Artificial Sequence
     453 <220> FEATURE:
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     467 <210> SEQ ID NO: 20
     469 <211> LENGTH: 28
     471 <212> TYPE: DNA
     473 <213> ORGANISM: Artificial Sequence
     477 <220> FEATURE:
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     485 <400> SEQUENCE: 20
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     491 <210> SEQ ID NO: 21
     493 <211> LENGTH: 14
     495 <212> TYPE: PRT
     497 <213> ORGANISM: Homo sapiens
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     503 Glu Asp Ala Val Asp Ala Glu Arg Leu Lys His Leu Ile Val
     505    1               5                  10
     511 <210> SEQ ID NO: 22
     513 <211> LENGTH: 1663
     515 <212> TYPE: PRT
     517 <213> ORGANISM: Homo sapiens
     521 <400> SEQUENCE: 22
     523 Met Gly Pro Thr Ser Gly Pro Ser Leu Leu Leu Leu Leu Leu Thr His
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525    1                        5                        10                       15
529 Leu Pro Leu Ala Leu Gly Ser Pro Met Tyr Ser Ile Ile Thr Pro Asn
531                 20                       25                       30
535 Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu Glu Ala His Asp
537           35                       40                       45
541 Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His Asp Phe Pro Gly
543        50                       55                       60
547 Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu Thr Pro Ala Thr
549 65                       70                       75                       80
553 Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala Asn Arg Glu Phe
555                 85                       90                       95
559 Lys Ser Glu Lys Gly Arg Asn Lys Phe Val Thr Val Gln Ala Thr Phe
561             100                      105                      110
565 Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser Leu Gln Ser Gly
567             115                      120                      125
571 Tyr Leu Phe Ile Gln Thr Asp Lys Thr Ile Tyr Thr Pro Gly Ser Thr
573        130                      135                      140
577 Val Leu Tyr Arg Ile Phe Thr Val Asn His Lys Leu Leu Pro Val Gly
579 145                      150                      155                      160
583 Arg Thr Val Met Val Asn Ile Glu Asn Pro Glu Gly Ile Pro Val Lys
585             165                      170                      175
589 Gln Asp Ser Leu Ser Ser Gln Asn Gln Leu Gly Val Leu Pro Leu Ser
591             180                      185                      190
595 Trp Asp Ile Pro Glu Leu Val Asn Met Gly Gln Trp Lys Ile Arg Ala
597             195                      200                      205
601 Tyr Tyr Glu Asn Ser Pro Gln Gln Val Phe Ser Thr Glu Phe Glu Val
603        210                      215                      220
607 Lys Glu Tyr Val Leu Pro Ser Phe Glu Val Ile Val Glu Pro Thr Glu
609 225                      230                      235                      240
613 Lys Phe Tyr Tyr Ile Tyr Asn Glu Lys Gly Leu Glu Val Thr Ile Thr
615             245                      250                      255
619 Ala Arg Phe Leu Tyr Gly Lys Lys Val Glu Gly Thr Ala Phe Val Ile
621             260                      265                      270
625 Phe Gly Ile Gln Asp Gly Glu Gln Arg Ile Ser Leu Pro Glu Ser Leu
627        275                      280                      285
631 Lys Arg Ile Pro Ile Glu Asp Gly Ser Gly Glu Val Val Leu Ser Arg
633        290                      295                      300
637 Lys Val Leu Leu Asp Gly Val Gln Asn Pro Arg Ala Glu Asp Leu Val
639 305                      310                      315                      320
643 Gly Lys Ser Leu Tyr Val Ser Ala Thr Val Ile Leu His Ser Gly Ser
645             325                      330                      335
649 Asp Met Val Gln Ala Glu Arg Ser Gly Ile Pro Ile Val Thr Ser Pro
651             340                      345                      350
655 Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met
657        355                      360                      365
661 Pro Phe Asp Leu Met Val Phe Val Thr Asn Pro Asp Gly Ser Pro Ala
663        370                      375                      380
667 Tyr Arg Val Pro Val Ala Val Gln Gly Glu Asp Thr Val Gln Ser Leu
669 385                      390                      395                      400
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/875,519

DATE: 09/06/2001
TIME: 10:53:04

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\09062001\I875519.raw**

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:397 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:397 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

9/6/01